Supporting Information

For

The Widespread Existence of Cytosine Methylation in Yeast DNA Measured by Gas Chromatography-Mass Spectrometry

Yang Tang¹, Xiang-Dong Gao², Yinsheng Wang³, Bi-Feng Yuan^{1*}, Yu-Qi Feng^{1*}

- Key Laboratory of Analytical Chemistry for Biology and Medicine (Ministry of Education), Department of Chemistry, Wuhan University, Wuhan 430072, P.R. China
- State Key Laboratory of Virology, College of Life Sciences, Wuhan University, Wuhan
 430072, P.R. China
- 3. Department of Chemistry, University of California, Riverside, CA 92521-0403.

*To whom correspondence should be addressed.

Tel.:+86-27-68755595; fax: +86-27-68755595.

E-mail address: bfyuan@whu.edu.cn; yqfeng@whu.edu.cn

Table S1. Linear range, regression data, limit of detection (LOD), and limit of quantification (LOQ) for the determination of 5mC by GC-MS.

Molar ratio	Linear range_ (%)	Calibration curve data			LOD	LOQ
		Slope	Intercept	R ² value	(pg)	(pg)
5mC/(5mC+Cytosine)	0.01-1.00	0.0045	-0.00003	0.9968	0.8	2.5

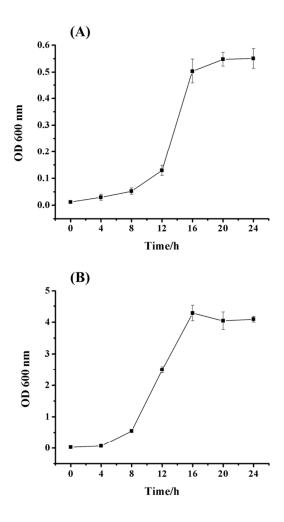


Figure S1. Cell growth curves of yeast strains. (A) *Yarrowia lipolytica* (CGMCC 2.1718). (B) *Saccharomyces cerevisiae* W1588-4C. Yeast cells were grown at 25°C and samples were taken after 0, 4, 8, 12, 16, 20, and 24 h culturing. OD_{600} values were determined after appropriate dilution with inoculated medium. Each data point was expressed by an average OD_{600} value with an error bar (i.e. standard deviation from three independent measurements).